

APPENDIX APRIMERS DESIGNED FOR DEN-2 CLONING/SEQUENCING PROJECT:

SEQ.

ID

| NO: | PRIMER | MER/SENSE | SEQUENCE |
|-----|------------------|-----------|---|
| 3 | pUC/M13-P5 | 25/+ | 5'-CCCACTCAGACGTTGTAAAACGAC-3' |
| 4 | pUC/M13-P5B | 27/+ | 5'-GGATGTGCTGCAAGGCCATTAAAGTTGG-3' |
| 5 | pUC/M13-P3 | 25/+ | 5'-TGAGCGGATAACAATTTACACAGG-3' |
| 6 | pUC/M13-P3B | 27/- | 5'-GGCTTTACACTTTATGCTTCCGGCTCG-3' |
| 7 | D2-1-Eco.T7 75/+ | | 5'-GCGGATATTG/GAATTC/TCTAGA/ AATTTAATACGACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3' (5'-Fill /EcoRI /XbaI/T7 Promoter/ 5'-end of DEN-2) |
| 8 | D2-SMT71 | 77/+ | 5'-CCAGT/GAATTC/GAGCTC/ACGCGT/ AAATTTAATACGACTCACTATA/ AGTTGTTAGTCTACGTGGACCGACAAAGACAG-3' (5'-Fill/EcoRI/SstI/MluI/T7 Promoter/ 5'-end of DEN-2) |
| 9 | D2-1 | 24/+ | 5'-AGTTGTTAGTCTACGTGGACCGAC-3' |
| 10 | D2-28 | 34/+ | 5'-GACAGATTCTTTGAGGGAGCTGAGCTCAACGTAG-3' |
| 11 | D2-134 | 28/+ | 5'-TCAATATGCTGAAACGGAGAGAAACCG-3' |
| 12 | cD2-250 | 26/- | 5'-GGGATTGTTAGGAAACGAAGGAACGC-3' |
| 13 | D2-274 | 32/+ | 5'-CCACCAACAGCAGGGATACTGAAAAGATGGGG-3' |
| 14 | cD2-378 | 25/- | 5'-TGCAGATCTGCGTCTCCTATTCAAG-3' |
| 15 | D2-528 | 25/+ | 5'-CGTGAACATGTGTACCCCTCATGGCC-3' |
| 16 | cD2-616 | 26/- | 5'-TTGCACCAACAGTCAATGTCTTCAGG-3' |
| 17 | D2-616 | 25/+ | 5'-ACCAGAAGACATAGATTGTTGGTGC-3' |
| 18 | cD2-618 | 25/- | 5'-GCACCAACAGTCTATGTCTTCTGGC-3' |
| 19 | cD2-771 | 25/- | 5'-ATGTTTCCAGGCCCTTCTGATGAC-3' |
| 20 | D2-847 | 25/+ | 5'-GCAGCAATCCTGGCATAACCATAG-3' |
| 21 | D2-996 | 27/+ | 5'-GGTTGACATAGTCTTAGAACATGGAAG-3' |
| 22 | cD2-996 | 27/- | 5'-CITCCATGTTCTAAGACTATGTCAACC-3' |

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| 23 | D2-1005 | 35/+ | 5'-GTCTTAGAACATGGAAGTTGTGTGACGACGATGGC-3' |
| 24 | D2-1141 | 25/+ | 5'-ACAACAGAATCTCGCTGCCCAACAC-3' |
| 25 | D2-1211 | 25/+ | 5'-GCAAACTCCATGGTAGACAGAGG-3' |
| 26 | cD2-1211 | 25/- | 5'-CCTCTGTCTACCATGGAGTGTTC-3' |
| 27 | cD2-1227 | 27/- | 5'-CCACATCCATTTCCCATCCTCTGTCT-3' |
| 28 | D2-1261 | 30/+ | 5'-GGAAAGGGAGGCATTGTGACCTGTGCTATG-3' |
| 29 | D2-1416 | 28/+ | 5'-GGAAATCAAATAACACCACAGAGTTCC-3' |
| 30 | cD2-1503 | 34/- | 5'-CTGCAGCAACACCATCTCATTGAAGTCGAGGCC-3' |
| 31 | D2-1510 | 25/+ | 5'-GACTTCAATGAGATGGTGTCTGTC-3' |
| 32 | cD2-1510 | 25/+ | 5'-GCAGCAGCACCATCTCATTGAAGTC-3' |
| 33 | D2-1546 | 28/+ | 5'-AAGCTTGGCTGGTGACAGGCAATGGTT-3' |
| 34 | cD2-1567 | 27/- | 5'-TGGTAACGGCAGGTCTAGGAACCATG-3' |
| 35 | D2-1777 | 23/+ | 5'-GGACATCTCAAGTCAGGCTGAG-3' |
| 36 | cD2-1777 | 23/+ | 5'-CTCAGCCTGCACCTTGAGATGTCC-3' |
| 37 | D2-1863 | 27/+ | 5'-GAAGGAAATAGCAGAAACACAACATGG-3' |
| 38 | cD2-1888 | 33/- | 5'-CCCTTCATATTGTACTCTGATAACTATTGTTC-3' |
| 39 | D2-2047 | 32/+ | 5'-CCTCCATTCCGAGACAGCTACATCATATAGG-3' |
| 40 | cD2-2047 | 32/- | 5'-CCTATGATGATGTAGCTGTCTCCGAATGGAGG-3' |
| 41 | D2-2170 | 29/+ | 5'-ATGGCCATTTAGGTGACACAGCCTGGGA-3' |
| 42 | cD2-2200 | 27/- | 5'-TGTAACACTCCTCCAGGGATCCAAA-3' |
| 43 | D2-2308 | 29/+ | 5'-CTCATAGGAGTCATTATCAGATGGATAGG-3' |
| 44 | cD2-2504 | 35/- | 5'-GGGGATTCTGGTTGGAACCTTATTTGTTCTGTCC-3' |
| 45 | cD2-2622 | 30/- | 5'-TGATTCAATTCTGGTGTATTGTTTCCAC-3' |
| 46 | D2-2702 | 25/+ | 5'-AAGGAATCATGCAGGCAGGAAAACG-3' |
| 47 | cD2-2864 | 22/- | 5'-ACTTCCAGCGAGTTCCAGCTC-3' A A |
| 48 | D2-2992 | 25/+ | 5'-AACAGAGCCCTCCATGCCGATATGG-3' |
| 49 | cD2-3105 | 22/- | 5'-TCCATTGCTCCAGGGGTGTGT-3' G |
| 50 | D2-3236 | 25/+ | 5'-AGCTTGAGATGGACTTTGATTCTG-3' |

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SEQ.
ID

NO: PRIMER

MER/SENSE

SEQUENCE

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| 51 | cD2-3410 | 22/- | 5'-GGTCTGATTTCATCCCGTACC-3' |
| 52 | D2-3621 | 23/+ | 5'-GTCCTTTAGAGACCTGGGAAGAG-3' |
| 53 | cD2-3739 | 25/- | 5'-GTTTCTCAAGAGTAGTCCAGCTGC-3' C |
| 54 | D2-3905 | 25/+ | 5'-ATCAATGGCAGTGACTATCATGGC-3' |
| 55 | cD2-4002 | 25/- | 5'-TGTTAAGAGCAGTGGAGAAACGGAC-3' A G |
| 56 | cD2-4060 | 25/- | 5'-GATTGAGACCTTTGATCGTCAACGC-3' |
| 57 | D2-4214 | 25/+ | 5'-TGACAGGACCATTAGTGGCTGGAGG-3' |
| 58 | D2-4257 | 34/+ | 5'-CGTGCTCACTGGACGATCGGCCGATTGGAACTG-3' |
| 59 | cD2-4323 | 24/- | 5'-GGGCTGCTTCTGATATTTCTGCC-3' C |
| 60 | D2-4497 | 25/+ | 5'-CCTGTGGGAAGTGAAGAAACAACGG-3' |
| 61 | cD2-4557 | 30/- | 5'-GCTCATCTTCCAGTTGAGCCTTTCCCATG-3' |
| 62 | cD2-4615 | 25/- | 5'-CTCCGGCTCCATCTGAGATATCC-3' G G A |
| 63 | D2-4746 | 25/+ | 5'-CCTAATATCATATGGAGGAGGCTGG-3' |
| 64 | D2-4792 | 25/+ | 5'-GAAGGAGAAGAGTCCAGGTATTGG-3' |
| 65 | cD2-4922 | 25/- | 5'-CTGTGAGCAATTGGAGATCCTGACG-3' T T |
| 66 | D2-4994 | 25/+ | 5'-GTGAGCATATGTGAGTGCTATAGC-3' |
| 67 | D2-5124 | 25/+ | 5'-TCTGACTATGCCCGAAGGTATCTC-3' |
| 68 | D2-5173 | 25/+ | 5'-ACATTAACTTTGGCCCCACTAGAG-3' |
| 69 | cD2-5272 | 19/- | 5'-CGATCTCCCGCCCGGTGTG-3' A |
| 70 | cD2-5318 | 25/- | 5'-CTAACTGGTGATAGCAGCCTCATGG-3' |
| 71 | cD2-5656 | 27/- | 5'-CCTACTGAGTTGTATCACTTTCTTTCC-3' |
| 72 | cD2-5891 | 26/- | 5'-TGGATTCTTCTTATTCTCCCTCTTC-3' |
| 73 | D2-5770 | 25/+ | 5'-TTCAAGGCTGAGAGGGTTATAGACC-3' |
| 74 | D2-6152 | 25/+ | 5'-TCTGGTGGCCTACAGAGTGGCAGC-3' |
| 75 | cD2-6252 | 27/- | 5'-CCTTCTTTTGTCCAGATTCCACTTCC-3' A |

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| NO: | PRIMER | MER/SENSE | SEQUENCE |
| 76 | D2-6493 | 35/+ | 5'-GGGTACAACCATGCTCTCAGTGAAGTGC CGGAGAC-3' |
| 77 | cD2-6605 | 24/- | 5'-TTCCCAGGGTCATCTTCCCTATAC-3' G |
| 78 | cD2-6624 | 31/- | 5'-GATGCTAGCCGTGATTATGCAGCACATTCCC-3' |
| 79 | D2-6748 | 25/+ | 5'-AAACAGAGAACACCCCAAGACAACC-3' |
| 80 | cD2-6932 | 21/- | 5'-CGGCATACAGCGTCCATGCTG-3' |
| 81 | D2-7055 | 25/+ | 5'-GTCTCGGGAAGGATGCCATTGTC-3' |
| 82 | cD2-7195 | 25/- | 5'-CTCTGGTTGCTTTTGCTTGAAGTCC-3' A G G |
| 83 | cD2-7217 | 27/- | 5'-CCGCCGCTGCTCTTTTCTGAGCTTCTC-3' |
| 84 | D2-7378 | 25/+ | 5'-AGGACTACATGGGCTCTGTGTGAGG-3' |
| 85 | cD2-7515 | 19/- | 5'-GAGAAGTCCAGCTCCGGCC-3' |
| 86 | D2-7769 | 25/+ | 5'-AGAGAAACATGGTCACACCAGAAGG-3' |
| 87 | cD2-7885 | 22/- | 5'-GTTCTTGGTGTCTCTGGTCTCC-3' |
| 88 | D2-8165 | 25/+ | 5'-GGAAATATGGAGGAGCCTAGTGAGG-3' |
| 89 | cD2-8210 | 22/- | 5'-ACCCAGTACATCTCATGTGTGG-3' |
| 90 | D2-8428 | 28/+ | 5'-GAGCATGAACATCATGGCACTATGACC-3' |
| 91 | D2-8440 | 25/+ | 5'-TCATGGCACTATGACCAAGACCACC-3' |
| 92 | cD2-8529 | 22/- | 5'-CAGTCTGACCACTCCGTTACCC-3' C A G |
| 93 | D2-8773 | 25/+ | 5'-AAGGTGAGAAGCAATGCAGCCTTGG-3' |
| 94 | D2-8798 | 29/+ | 5'-GGGCCATATTCACTGATGAGAACAAGTGG-3' |
| 95 | cD2-8865 | 22/- | 5'-TCTTTCCCTGTCAACCAGCTCC-3' C T |
| 96 | D2-9046 | 25/+ | 5'-AATGAAGATCACTGGTTCTCCAGAG-3' |
| 97 | D2-9131 | 25/+ | 5'-ACGTGAGCAAGAAAGAGGGAGGAGC-3' |
| 98 | cD2-9166 | 22/- | 5'-TGTCCCATCCTGCTGTGTATC-3' A G |
| 99 | cD2-9234 | 30/- | 5'-GCTAGTTTCTGTGTTCTCCTTCCATGTGG-3' |
| 100 | D2-9344 | 25/+ | 5'-TCATATCGAGAAGAGACCAAGAGG-3' |
| 101 | cD2-9429 | 24/- | 5'-ACTCCTTCTCCCTCCATCTGTCTG-3' |

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| NO. | PRIMER | MER/SENSE | SEQUENCE |
| 102 | CD2-9438 | 27/- | 5'-ATGCTTTTGAAGATTCTTCTCCCTCC-3' A C |
| 103 | CD2-9468 | 32/- | 5'-GCACAGCGATTCTTCTGTGATTGTTAGGTGC-3' |
| 104 | D2-9645 | 25/+ | 5'-ACAATGGGAACCTTCAAGAGGATGG-3' |
| 105 | D2-9656.BAM | 45/+ | 5'-TTATCACATT/GGATCC/TTCAAGAGGATGGA ATGATTGGACACAAG-3' (5'-Fill/BamHI/DEN-2 Sequence) |
| 106 | CD2-9668 | 28/- | 5'-CAGAAGGGCACTTGTGTCCAATCATTC-3' |
| 107 | CD2-9779 | 21/- | 5'-CTCCCTGGGAATTCCGGCTC-3' T G |
| 108 | CD2-9796 | 28/- | 5'-CCGTCTCCCGCAAAGACCACCTGCTCC-3' |
| 109 | CD2-9796.XBA | 44/- | 5'-TTATCACCTA/TCTAGA/CCGTCTCCC GCAAAGACCACCTGCTCC-3' |
| 110 | CD2-9913 | 26/- | 5'-GTTGGAACCAATGTGATGGTACTGC-3' |
| 111 | D2-9937 | 25/+ | 5'-ACAAGTCGAACAACCTGCTCCATAC-3' |
| 112 | CD2-9977 | 21/- | 5'-GCATGCTTCCGTGCTCATCC-3' T |
| 113 | CD2-10003 | 25/- | 5'-CTTGAATCCACACCTGTTCCAGAC-3' |
| 114 | D2-10203 | 25/+ | 5'-ATACACAGATTACATGCCATCCATG-3' |
| 115 | CD2-10261 | 21/- | 5'-TTTTCCTTCTACCACAGGAC-3' T A |
| 116 | D2-10289 | 25/- | 5'-GAAACAAGGCTAGAAGTCAGGTCGG-3' |
| 117 | CD2-10337 | 23/- | 5'-GACGGGGCTCACAGGTAGCATAG-3' |
| 118 | D2-10418 | 25/+ | 5'-GCCTGTAGCTCCACCTGAGAAGGTG-3' |
| 119 | D2-10470 | 25/+ | 5'-GGAAGCTGTACGCATGGCGTAGTGG-3' |
| 120 | CD2-10530 | 19/- | 5'-GGGCCCCGTTGTTGCTGC-3' A |
| 121 | CD2-10687 | 59/- | 5'-AGAACCTGTTGATTCAACAGCACCATTCCATTTCTG-3' |
| 122 | CD2-10687.XBA | 59/- | 5'-TTATCACCTA/GCATGC/TCTAGA/ AGAACCTGTTGATTCAACAGCACCATTCCATTTCTG-3' (5'-Fill/SphI/XbaI/ 3'-End DEN-2 Sequence) |
| 123 | CD2-10687.X2 | 52/- | 5'-TTATCACCTA/TCTAGA/ GAACCTGTTGATTCAACAGCACCATTCCATTTCTG-3' (5'-Fill/XbaI/ 3'-End DEN-2 Sequence) |